

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Ingham, Phillip W.
McMahon, Andrew P.
Tabin, Clifford J.

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(ii) TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
Proteins and Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 47

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street
(C) CITY: Boston
(D) STATE: MA
20 (E) COUNTRY: USA
(F) ZIP: 02109

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII(text)

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(vi) CURRENT APPLICATION DATA:

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(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/435,093
(B) FILING DATE: 4-MAY-1995

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/356,060
(B) FILING DATE: 14-DEC-1994

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/176,427
(B) FILING DATE: 30-DEC-1993

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709
(C) REFERENCE/DOCKET NUMBER: HMI-006CP3

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
(B) TELEFAX: (617) 227-5941

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

10 (A) NAME/KEY: CDS
(B) LOCATION: 1..1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15	ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile 1 5 10 15	48
20	TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly 20 25 30	96
25	ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys 35 40 45	144
30	CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg 50 55 60	192
35	TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr 65 70 75 80	240
40	CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly 85 90 95	288
45	GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu 100 105 110	336
50	GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr 115 120 125	384
55	GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr 130 135 140	432
60	GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys 145 150 155 160	480
65	TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val 165 170 175	528

	TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn 180 . . . 185 . . . 190	576
5	TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val 195 . . . 200 . . . 205	624
10	CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly 210 . . . 215 . . . 220	672
15	GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp 225 . . . 230 . . . 235 . . . 240	720
20	TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr 245 . . . 250 . . . 255	768
	GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala 260 . . . 265 . . . 270	816
25	CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly 275 . . . 280 . . . 285	864
30	TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln 290 . . . 295 . . . 300	912
35	CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser 305 . . . 310 . . . 315 . . . 320	960
	GTC CAC AGC GTC TCA TTG CGG GAG GCG TCC GGA GCC TAC GCC CCA Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro 325 . . . 330 . . . 335	1008
40	CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys 340 . . . 345 . . . 350	1056
45	TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro 355 . . . 360 . . . 365	1104
50	TTC CGC TTG GCT CAG GGG CTG CTG GCC CTC TGC CCA GAT GGG GCC Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala 370 . . . 375 . . . 380	1152
	ATC CCT ACT GCC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg	1200
55	385 . . . 390 . . . 395 . . . 400	
	CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His	1248

405

410

415

CCG CTG GGC ATG GTG GCA CCG GCC AGC TG
 Pro Leu Gly Met Val Ala Pro Ala Ser
 5 420 425

1277

(2) INFORMATION FOR SEQ ID NO:2:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

20 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1191

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	48
1 5 10 15	
30 GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	96
20 25 30	
35 CCG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	144
35 40 45	
40 GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	192
50 55 60	
45 GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	240
65 70 75 80	
50 TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	288
85 90 95	
55 CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	336
100 105 110	
55 GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	384
115 120 125	

	TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly 130 135 140	432
5	CGT GCC TTG GAC ATC ACC ACG TCT GAC CGT GAC CGT AAT AAG TAT GGT Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly 145 150 155 160	480
10	TTG TTG GCG CGC CTA GCT GTG GAA GCC GGA TTC GAC TGG GTC TAC TAC Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr 165 170 175	528
15	GAG TCC CGC AAC CAC ATC CAC GTA TCG GTC AAA GCT GAT AAC TCA CTG Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu 180 185 190	576
20	GCG GTC CGA GCC GGA GGC TGC TTT CCG GGA AAT GCC ACG GTG CGC TTG Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu 195 200 205	624
25	CGG AGC GGC GAA CGG AAG GGG CTG AGG GAA CTA CAT CGT GGT GAC TGG Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp 210 215 220	672
30	GTA CTG GCC GCT GAT GCA GCG GGC CGA GTG GTA CCC ACG CCA GTG CTG Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu 225 230 235 240	720
35	CTC TTC CTG GAC CGG GAT CTG CAG CGC CGC GCC TCG TTC GTG GCT GTG Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val 245 250 255	768
40	GAG ACC GAG CGG CCT CCG CGC AAA CTG TTG CTC ACA CCC TGG CAT CTG Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu 260 265 270	816
45	GTG TTC GCT CGC GGG CCA GCG CCT GCT CCA GGT GAC TTT GCA CCG Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro 275 280 285	864
50	GTG TTC GCG CGC TTA CGT GCT GGC GAC TCG GTG CTG GCT CCC GGC Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly 290 295 300	912
55	GGG GAC GCG CTC CAG CCG GCG CGC GTA GCC CGC GTG GCG CGC GAG GAA Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu 305 310 315 320	960
60	GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val 325 330 335	1008
65	AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp 340 345 350	1056
70	GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala	1104

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360

365

CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT
Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
5 370 375 380

1152

CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG
Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
10 385 390 395

1190

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
25 (B) LOCATION: 1..1233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

30 ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15

48

35 CTG CTG CTG CTT CTG GTG CCG GCG CGG GGC TGC GGG CCG GGC CGG
Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30

96

40 GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC
Val Val Gly Ser Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

144

45 TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC
Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

192

50 GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

240

55 CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC
Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

288

55 ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

336

-151-

TCA CTG GCC ATC TCT GTC ATG AAC CAG TGG CCT GGT GTG AAA CTG CGG	3.84
Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg	
115 120 125	
5 GTG ACC GAA GGC CGG GAT GAA GAT GGC CAT CAC TCA GAG GAG TCT TTA	432
Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu	
130 135 140	
10 CAC TAT GAG GGC CGC GCG GTG GAT ATC ACC ACC TCA GAC CGT GAC CGA	480
His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg	
145 150 155 160	
15 AAT AAG TAT GGA CTG CTG GCG CGC TTA GCA GTG GAG GCC GGC TTC GAC	528
Asn Lys Tyr Glu Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp	
165 170 175	
20 TGG GTG TAT TAC GAG TCC AAG GCC CAC GTG CAT TGC TCT GTC AAG TCT	576
Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser	
180 185 190	
25 GAG CAT TCG GCC GCT GCC AAG ACA GGT GGC TGC TTT CCT GCC GGA GCC	624
Glu His Ser Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala	
195 200 205	
30 CAG GTG CGC CTA GAG AAC GGG GAG CGT GTG GCC CTG TCA GCT GTA AAG	672
Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys	
210 215 220	
35 CCA GGA GAC CGG GTG CTG GCC ATG GGG GAG GAT GGG ACC CCC ACC TTC	720
Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe	
225 230 235 240	
40 AGT GAT GTG CTT ATT TTC CTG GAC CGC GAG CCA AAC CGG CTG AGA GCT	768
Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala	
245 250 255	
45 TTC CAG GTC ATC GAG ACT CAG GAT CCT CCG CGT CGG CTG GCG CTC ACG	816
Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr	
260 265 270	
50 CCT GCC CAC CTG CTC ATT GCG GAC AAT CAT ACA GAA CCA GCA GCC	864
Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala	
275 280 285	
55 CAC TTC CGG GCC ACA TTT GCC AGC CAT GTG CAA CCA GGC CAA TAT GTG	912
His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val	
290 295 300	
60 CTG GTA TCA GGG GTA CCA GGC CTC CAG CCT GCT CGG GTG GCA GCT GTC	960
Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val	
305 310 315 320	
65 TCC ACC CAC GTG GCC CTT GGG TCC TAT GCT CCT CTC ACA AGG CAT GGG	1008
Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly	
325 330 335	
70 ACA CTT GTG GTG GAG GAT GTG GTG GCC TCC TGC TTT GCA GCT GTG GCT	1056
Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala	

340

345

350

GAC CAC CAT CTG GCT CAG TTG GCC TTC TGG CCC CTG CGA CTG TTT CCC
Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
5 355 360 365 1104

AGT TTG GCA TGG GGC AGC TGG ACC CCA AGT GAG GGT GTT CAC TCC TAC
Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
10 370 375 380 1152

CCT CAG ATG CTC TAC CGC CTG GGG CGT CTC TTG CTA GAA GAG AGC ACC
Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr
385 390 395 400 1200

TTC CAT CCA CTG GGC ATG TCT GGG GCA GGA AGC TGAAGGGACT CTAACCACTG
Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
15 405 410 1253

CCCTCCTGGA ACTGCTGTGC GTGGATCC 20 1281

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

35 (A) NAME/KEY: CDS
(B) LOCATION: 1..1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 ATG CTG CTG CTG CTG GCC AGA TGT TTT CTG GTG ATC CTT GCT TCC TCG
Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
1 5 10 15 48

45 CTG CTG GTG TGC CCC GGG CTG GCC TGT GGG CCC GGC AGG GGG TTT GGA
Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
20 25 30 96

50 AAG AGG CGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT
Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
35 40 45 144

ATT CCC AAC GTA GCC GAG AAG ACC CTA GGG GCC AGC GGC AGA TAT GAA
Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
50 55 60 192

55 GGG AAG ATC ACA AGA AAC TCC GAA CGA TTT AAG GAA CTC ACC CCC AAT
Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
65 70 75 80 240

150

5	TAC AAC CCC GAC ATC ATA TTT AAG GAT GAG GAA AAC ACG GGA GCA GAC Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp 85 90 95	288
10	CGG CTG ATG ACT CAG AGG TGC AAA GAC AAG TTA AAT GCC TTG GCC ATC Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile 100 105 110	336
15	TCT GTG ATG AAC CAG TGG CCT GGA GTG AGG CTG CGA GTG ACC GAG GGC Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly 115 120 125	384
20	TGG GAT GAG GAC GGC CAT CAT TCA GAG GAG TCT CTA CAC TAT GAG GGT Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly 130 135 140	432
25	CGA GCA GTG GAC ATC ACC ACG TCC GAC CGG GAC CGC AGC AAG TAC GGC Arg Ala Val Asp Ile Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly 145 150 155 160	480
30	ATG CTG GCT CGC CTG GCT GTG GAA GCA GGT TTC GAC TGG GTC TAC TAT Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr 165 170 175	528
35	GAA TCC AAA GCT CAC ATC CAC TGT TCT GTG AAA GCA GAG AAC TCC GTG Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val 180 185 190	576
40	GCG GCC AAA TCC GGC GGC TGT TTC CCG GGA TCC GCC ACC GTG CAC CTG Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu 195 200 205	624
45	GAG CAG GGC GGC ACC AAG CTG GTG AAG GAC TTA CGT CCC GGA GAC CGC Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg 210 215 220	672
50	GTG CTG GCG GCT GAC CAG GGC CGG CTG CTG TAC AGC GAC TTC CTC Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu 225 230 235 240	720
55	ACC TTC CTG GAC CGC GAC GAA GGC GCC AAG AAG GTC TTC TAC GTG ATC Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile 245 250 255	768
60	GAG ACG CTG GAG CCG CGC GAG CGC CTG CTG CTC ACC GCC GCG CAC CTG Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu 260 265 270	816
65	CTC TTC GTG GCG CCG CAC AAC GAC TCG GGG CCC ACG CCC GGG CCA AGC Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser 275 280 285	864
70	GCG CTC TTT GCC AGC CGC GTG CGC CCC GGG CAG CGC GTG TAC GTG GTG Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val 290 295 300	912
75	GCT GAA CGC GGC GGG GAC CGC CGG CTG CTG CCC GCC GCG GTG CAC AGC	960

154

Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser					
305	310	315	320		
GTG ACG CTG CGA GAG GAG GCG GGC GCG TAC GCG CCG CTC ACG GCG				1008	
5	Val Thr Leu Arg Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala				
	325	330	335		
CAC GGC ACC ATT CTC ATC AAC CGG GTG CTC GCC TCG TGC TAC GCT GTC				1056	
	His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val				
10	340	345	350		
ATC GAG GAG CAC AGC TGG GCA CAC CGG GCC TTC GCG CCT TTC CGC CTG				1104	
	Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu				
	355	360	365		
15	GCG CAC GCG CTG CTG GCC GCG CTG GCA CCC GCC CGC ACG GAC GGC GGG			1152	
	Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly				
	370	375	380		
20	GGC GGG GGC AGC ATC CCT GCA GCG CAA TCT GCA ACG GAA GCG AGG GGC			1200	
	Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly				
	385	390	395	400	
25	GCG GAG CCG ACT GCG GGC ATC CAC TGG TAC TCG CAG CTG CTC TAC CAC			1248	
	Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His				
	405	410	415		
30	ATT GGC ACC TGG CTG TTG GAC AGC GAG ACC ATG CAT CCC TTG GGA ATG			1296	
	Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met				
	420	425	430		
GCG GTC AAG TCC AGC TG				1313	
	Ala Val Lys Ser Ser				
	435				
35					
(2) INFORMATION FOR SEQ ID NO:5:					
(i) SEQUENCE CHARACTERISTICS:					
40	(A) LENGTH: 1256 base pairs				
	(B) TYPE: nucleic acid				
	(C) STRANDEDNESS: both				
	(D) TOPOLOGY: linear				
45	(ii) MOLECULE TYPE: cDNA				
(ix) FEATURE:					
50	(A) NAME/KEY: CDS				
	(B) LOCATION: 1..1257				
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:					
55	ATG CGG CTT TTG ACG AGA GTG CTG CTG GTG TCT CTT CTC ACT CTG TCC				48
	Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser				
	1	5	10	15	

TTG GTG GTG TCC GGA CTG GCC TGC GGT CCT GGC AGA GGC TAC GGC AGA	96
Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg	
20 25 30	
5 AGA AGA CAT CCG AAG AAG CTG ACA CCT CTC GCC TAC AAG CAG TTC ATA	144
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
35 40 45	
10 CCT AAT GTC GCG GAG AAG ACC TTA GGG GCC AGC GGC AGA TAC GAG GGC	192
Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
50 55 60	
15 AAG ATA ACG CGC AAT TCG GAG AGA TTT AAA GAA CTT ACT CCA AAT TAC	240
Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	
65 70 75 80	
20 AAT CCC GAC ATT ATC TTT AAG GAT GAG GAG AAC ACG GGA GCG GAC AGG	288
Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg	
85 90 95	
25 CTC ATG ACA CAG AGA TGC AAA GAC AAG CTG AAC TCG CTG GCC ATC TCT	336
Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser	
100 105 110	
30 GTA ATG AAC CAC TGG CCA GGG GTT AAG CTG CGT GTG ACA GAG GGC TGG	384
Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp	
115 120 125	
35 GAT GAG GAC GGT CAC CAT TTT GAA GAA TCA CTC CAC TAC GAG GGA AGA	432
Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg	
130 135 140	
40 GCT GTT GAT ATT ACC ACC TCT GAC CGA GAC AAG AGC AAA TAC GGG ACA	480
Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr	
145 150 155 160	
45 CTG TCT CGC CTA GCT GTG GAG GCT GGA TTT GAC TGG GTC TAT TAC GAG	528
Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu	
165 170 175	
50 TCC AAA GCC CAC ATT CAT TGC TCT GTC AAA GCA GAA AAT TCG GTT GCT	576
Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala	
180 185 190	
55 GCG AAA TCT GGG GGC TGT TTC CCA GGT TCG GCT CTG GTC TCG CTC CAG	624
Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln	
195 200 205	
60 GAC GGA GGA CAG AAG GCC GTG AAG GAC CTG AAC CCC GGA GAC AAG GTG	672
Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val	
210 215 220	
65 CTG GCG GCA GAC AGC GCG GGA AAC CTG GTG TTC AGC GAC TTC ATC ATG	720
Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met	
225 230 235 240	
70 TTC ACA GAC CGA GAC TCC ACG ACG CGA CGT GTG TTT TAC GTC ATA GAA	768
Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu	

150

	245	250	255			
5	ACG CAA GAA CCC GTT GAA AAG ATC ACC CTC ACC GCC GCT CAC CTC CTT Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu	260	265	270	816	
10	TTT GTC CTC GAC AAC TCA ACG GAA GAT CTC CAC ACC ATG ACC GCC GCG Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala	275	280	285	864	
15	TAT GCC AGC AGT GTC AGA GCC GGA CAA AAG GTG ATG GTT GAT GAT Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp	290	295	300	912	
20	AGC GGT CAG CTT AAA TCT GTC ATC GTG CAG CGG ATA TAC ACG GAG GAG Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu	305	310	315	320	960
25	CAG CGG GGC TCG TTC GCA CCA GTG ACT GCA CAT GGG ACC ATT GTG GTC Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val	325	330	335	1008	
30	GAC AGA ATA CTG GCG TCC TGT TAC GCC GTA ATA GAG GAC CAG GGG CTT Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu	340	345	350	1056	
35	GCG CAT TTG GCC TTC GCG CCC GCC AGG CTC TAT TAT TAC GTG TCA TCA Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Val Ser Ser	355	360	365	1104	
40	TTC CTG TCC CCC AAA ACT CCA GCA GTC GGT CCA ATG CGA CTT TAC AAC Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	370	375	380	1152	
45	AGG AGG GGG TCC ACT GGT ACT CCA GGC TCC TGT CAT CAA ATG GGA ACG Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	385	390	395	400	1200
	TGG CTT TTG GAC AGC AAC ATG CTT CAT CCT TTG GGG ATG TCA GTA AAC Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn	405	410	415	1248	
	TCA AGC TG Ser Ser				1256	

(2) INFORMATION FOR SEQ ID NO:6:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1425

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG	CTG	CTG	CTG	GCG	AGA	TGT	CTG	CTG	CTA	GTC	CTC	GTC	TCC	TCG	CTG	48	
Met	Leu	Leu	Leu	Ala	Arg	Cys	Leu	Leu	Leu	Val	Leu	Val	Ser	Ser	Leu		
10	1						5			10				15			
CTG	GTA	TGC	TCG	GGA	CTG	GCG	TGC	GGA	CCG	GGC	AGG	GGG	TTC	GGG	AAG	96	
Leu	Val	Cys	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	Lys		
15					20				25				30				
AGG	AGG	CAC	CCC	AAA	AAG	CTG	ACC	CCT	TTA	GCC	TAC	AAG	CAG	TTT	ATC	144	
Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phé	Ile		
35					35				40			45					
CCC	AAT	GTG	GCC	GAG	AAG	ACC	CTA	GGC	GCC	AGC	GGA	AGG	TAT	GAA	GGG	192	
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly		
20					50			55			60						
AAG	ATC	TCC	AGA	AAC	TCC	GAG	CGA	TTT	AAG	GAA	CTC	ACC	CCC	AAT	TAC	240	
Lys	Ile	Ser	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr		
25					65			70			75			80			
AAC	CCC	GAC	ATC	ATA	TTT	AAG	GAT	GAA	GAA	AAC	ACC	GGA	GCG	GAC	AGG	288	
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg		
30					85			90			95						
CTG	ATG	ACT	CAG	AGG	TGT	AAG	GAC	AAG	TTG	AAC	GCT	TTG	GCC	ATC	TCG	336	
Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	Ser		
35					100			105			110						
GTG	ATG	AAC	CAG	TGG	CCA	GGA	GTG	AAA	CTG	CGG	GTG	ACC	GAG	GGC	TGG	384	
Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp		
					115			120			125						
GAC	GAA	GAT	GGC	CAC	CAC	TCA	GAG	GAG	TCT	CTG	CAC	TAC	GAG	GGC	CGC	432	
Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg		
40					130			135			140						
GCA	GTG	GAC	ATC	ACC	ACG	TCT	GAC	CGC	GAC	CGC	AGC	AAG	TAC	GGC	ATG	480	
45	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	Met	
					145			150			155			160			
CTG	GCC	CGC	CTG	GCG	GTG	GAG	GCC	GGC	TTC	GAC	TGG	GTG	TAC	TAC	GAG	528	
Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu		
50					165			170			175						
TCC	AAG	GCA	CAT	ATC	CAC	TGC	TCG	GTG	AAA	GCA	GAG	AAC	TCG	GTG	GCG	576	
Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala		
55					180			185			190						
GCC	AAA	TCG	GGA	GGC	TGC	TTC	CCG	GGC	TCG	GCC	ACG	GTG	CAC	CTG	GAG	624	
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	Glu		
					195			200			205						

	CAG GGC GGC ACC AAG CTG GTG AAG GAC CTG AGC CCC GGG GAC CGC GTG		672
	Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val		
5	210 215 220		
	CTG GCG GCG GAC GAC CAG GGC CGG CTG CTC TAC AGC GAC TTC CTC ACT		720
	Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr		
	225 230 235 240		
10	TTC CTG GAC CGC GAC GAC GGC GCC AAG AAG GTC TTC TAC GTG ATC GAG		768
	Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu		
	245 250 255		
15	ACG CGG GAG CCG CGC GAG CGC CTG CTG CTC ACC GCC GCG CAC CTG CTC		816
	Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu		
	260 265 270		
20	TTT GTG GCG CCG CAC AAC GAC TCG GCC ACC GGG GAG CCC GAG GCG TCC		864
	Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser		
	275 280 285		
25	TCG GGC TCG GGG CCG CCT TCC GGG GGC GCA CTG GGG CCT CGG GCG CTG		912
	Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu		
	290 295 300		
30	TTC GCC AGC CGC GTG CGC CCG GGC CAG CGC GTG TAC GTG GTG GCC GAG		960
	Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu		
	305 310 315 320		
35	CGT GAC GGG GAC CGC CGG CTC CTG CCC GCC GCT GTG CAC AGC GTG ACC		1008
	Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr		
	325 330 335		
40	CTA AGC GAG GAG GCC GCG GGC GCC TAC GCG CCG CTC ACG GCC CAG GGC		1056
	Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly		
	340 345 350		
45	ACC ATT CTC ATC AAC CGG GTG CTG GCC TCG TGC TAC GCG GTC ATC GAG		1104
	Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu		
	355 360 365		
50	GAG CAC AGC TGG GCG CAC CGG GCC TTC GCG CCC TTC CGC CTG GCG CAC		1152
	Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His		
	370 375 380		
55	GCG CTC CTG GCT GCA CTG GCG CCC GCG CGC ACG GAC CGC GGC GGG GAC		1200
	Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp		
	385 390 395 400		
60	AGC GGC GGC GGG GAC CGC GGG GGC GGC GGC AGA GTA GCC CTA ACC		1248
	Ser Gly Gly Asp Arg Gly Gly Gly Gly Arg Val Ala Leu Thr		
	405 410 415		
65	GCT CCA GGT GCT GCC GAC GCT CCG GGT GCG GGG GCC ACC GCG GGC ATC		1296
	Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile		
	420 425 430		
70	CAC TGG TAC TCG CAG CTG CTC TAC CAA ATA GGC ACC TGG CTC CTG GAC		1344

His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445

5 AGC GAG GCC CTG CAC CCG CTG GGC ATG GCG GTC AAG TCC AGC NNN AGC 1392
 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460

10 CGG GGG GCC GGG GGA GGG GCG CGG GAG GGG GCC 1425
 Arg Gly Ala Gly Gly Ala Arg Glu Gly Ala
 465 470 475

(2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..939

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGG CGC CTC ATG ACC CAG CGC TGC AAG GAC CGC CTG AAC TCG CTG GCT 48
 Arg Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu Ala
 1 5 10 15

35 ATC TCG GTG ATG AAC CAG TGG CCC GGT GTG AAG CTG CGG GTG ACC GAG 96
 Ile Ser Val Met Asn Gin Trp Pro Gly Val Lys Leu Arg Val Thr Glu
 20 25 30

40 GGC TGG GAC GAG GAC GGC CAC CAC TCA GAG GAG TCC CTG CAT TAT GAG 144
 Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu
 35 40 45

45 GGC CGC GCG GTG GAC ATC ACC ACA TCA GAC CGC GAC CGC AAT AAG TAT 192
 Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr
 50 55 60

50 GGA CTG CTG GCG CGC TTG GCA GTG GAG GCC GGC TTT GAC TGG GTG TAT 240
 Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr
 65 70 75 80

55 TAC GAG TCA AAG GCC CAC GTG CAT TGC TCC GTC AAG TCC GAG CAC TCG 288
 Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His Ser
 85 90 95

55 GCC GCA GCC AAG ACG GGC GGC TGC TTC CCT GCC GGA GCC CAG GTA CGC 336
 Ala Ala Ala Lys Thr Gly Gly Cys Ser Phe Pro Ala Gly Ala Gln Val Arg
 100 105 110

CTG GAG AGT GGG GCG CGT GTG GCC TTG TCA GCC GTG AGG CCG GGA GAC Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly Asp 115 120 125	384
5 CGT GTG CTG GCC ATG GGG GAG GAT GGG AGC CCC ACC TTC AGC GAT GTG Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp Val 130 135 140	432
10 CTC ATT TTC CTG GAC CGC GAG CCC CAC AGG CTG AGA GCC TTC CAG GTC Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln Val 145 150 155 160	480
15 ATC GAG ACT CAG GAC CCC CCA CGC CGC CTG GCA CTC ACA CCC GCT CAC Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala His 165 170 175	528
20 CTG CTC TTT ACG GCT GAC AAT CAC ACG GAG CCG GCA GCC CGC TTC CGG Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe Arg 180 185 190	576
25 GCC ACA TTT GCC AGC CAC GTG CAG CCT GGC CAG TAC GTG CTG GTG GCT Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val Ala 195 200 205	624
30 GGG GTG CCA GGC CTG CAG CCT GCC CGC GTG GCA GCT GTC TCT ACA CAC Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr His 210 215 220	672
35 GTG GCC CTC GGG GCC TAC GCC CCG CTC ACA AAG CAT GGG ACA CTG GTG Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu Val 225 230 235 240	720
40 CTG GAG GAT GTG GTG GCA TCC TGC TTC GCG GCC GTG GCT GAC CAC CAC Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His His 245 250 255	768
45 CTG GCT CAG TTG GCC TTC TGG CCC CTG AGA CTC TTT CAC AGC TTG GCA Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu Ala 260 265 270	816
50 TGG GGC AGC TGG ACC CCG GGG GAG GGT GTG CAT TGG TAC CCC CAG CTG Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln Leu 275 280 285	864
55 CTC TAC CGC CTG GGG CGT CTC CTG CTA GAA GAG GGC AGC TTC CAC CCA Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser Phe His Pro 290 295 300	912
50 CTG GGC ATG TCC GGG GCA GGG AGC TGA Leu Gly Met Ser Gly Ala Gly Ser Xaa 305 310	939

(2) INFORMATION FOR SEQ ID NO:8:

55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
10 1 5 10 15

Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
20 25 30

Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
15 35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
20 50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
25 65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
25 85 90 95

Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
30 100 105 110

Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
35 115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
40 145 150 155 160

Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
40 165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
45 180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
45 195 200 205

His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
50 210 215 220

Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
55 225 230 235 240

Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
55 245 250 255

Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
55 260 265 270

His Leu Leu Phe Val Ala-Pro Gln His Asn Gln Ser Glu Ala Thr Gly
275 280 285

5 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
290 295 300

Arg Val Tyr Val Leu Gly Glu Gly Gln Leu Leu Pro Ala Ser
305 310 315 320

10 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
325 330 335

Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
15 340 345 350

Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
355 360 365

20 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
370 375 380

Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
385 390 395 400

25 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
405 410 415

Pro Leu Gly Met Val Ala Pro Ala Ser
30 420 425

(2) INFORMATION FOR SEQ ID NO:9:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15

50 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
20 25 30

Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45

55 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
50 55 60

Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn

65.	70	75	80
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp			
	85	90	95
5			
	Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile		
	100	105	110
10	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly		
	115	120	125
	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly		
	130	135	140
15	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly		
	145	150	155
	Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr		
20	165	170	175
	Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu		
	180	185	190
25	Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu		
	195	200	205
	Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp		
	210	215	220
30	Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu		
	225	230	240
	Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val		
	245	250	255
35	Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu		
	260	265	270
40	Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro		
	275	280	285
	Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly		
	290	295	300
45	Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu		
	305	310	315
	Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val		
	325	330	335
50	Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp		
	340	345	350
55	Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala		
	355	360	365
	Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser		
	370	375	380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
385 390 395

5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 411 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30

25 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

30 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

35 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

40 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125

Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140

45 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145 150 155 160

50 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
180 185 190

55 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
195 200 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys

210 215 220
Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
225 230 235 240
5 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
245 250 255
Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
10 260 265 270
Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
275 280 285
15 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
290 295 300
Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
305 310 315 320
20 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
325 330 335
Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
25 340 345 350
Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
355 360 365
30 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
370 375 380
Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr
385 390 395 400
35 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
405 410
40 (2) INFORMATION FOR SEQ ID NO:11:
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 437 amino acids
47 (B) TYPE: amino acid
48 (D) TOPOLOGY: linear
50 (ii) MOLECULE TYPE: protein
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
1 5 10 15
55 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
20 25 30

Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
35 40 45

5 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
50 55 60

Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
65 70 75 80

10 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
85 90 95

Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
100 105 110

15 Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
20 130 135 140

Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly
145 150 155 160

25 Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
165 170 175

Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val
180 185 190

30 Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu
195 200 205

Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg
35 210 215 220

Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu
225 230 235 240

40 Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile
245 250 255

Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu
45 260 265 270

Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser
275 280 285

50 Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val
290 295 300

Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser
305 310 315 320

55 Val Thr Leu Arg Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala
325 330 335

His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val

340

345

350

Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
355 360 365

5

Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
370 375 380

10 Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
385 390 395 400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
405 410 415

15 Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
420 425 430

Ala Val Lys Ser Ser
435

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 418 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

35 Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

40 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

45 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

50 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

55 Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

5 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
145 150 155 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

10 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
195 200 205

15 Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
210 215 220

Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
20 225 230 235 240

Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
245 250 255

25 Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
260 265 270

Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
275 280 285

30 Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
290 295 300

Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
35 305 310 315 320

Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
325 330 335

40 Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
340 345 350

Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Val Ser Ser
355 360 365

45 Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
370 375 380

50 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
385 390 395 400

Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
405 410 415

55 Ser Ser

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 475 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Val Ser Ser Leu
15 1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
20 25 30

20 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
25 50 55 60

Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

30 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ile Ser
100 105 110

35 Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
40 130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
145 150 155 160

45 Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
180 185 190

50 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
195 200 205

Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
210 215 220

55 Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
225 230 235 240

Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
 245 250 255

5 Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
 260 265 270

Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
 275 280 285

10 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
 290 295 300

Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
 305 310 315 320

15 Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
 325 330 335

Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
 20 340 345 350

Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
 355 360 365

25 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
 370 375 380

Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
 385 390 395 400

30 Ser Gly Gly Asp Arg Gly Gly Gly Arg Val Ala Leu Thr
 405 410 415

Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
 35 420 425 430

His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445

40 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460

Arg Gly Ala Gly Gly Ala Arg Glu Gly Ala
 465 470 475

45

(2) INFORMATION FOR SEQ ID NO:14:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu Ala
1 5 10 15

5 Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu
20 25 30

Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu
35 40 45

10 Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr
50 55 60

Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr
15 65 70 75 80

Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His Ser
85 90 95

20 Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val Arg
100 105 110

Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly Asp
115 120 125

25 Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp Val
130 135 140

Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln Val
30 145 150 155 160

Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala His
165 170 175

35 Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe Arg
180 185 190

Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val Ala
195 200 205

40 Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr His
210 215 220

Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu Val
45 225 230 235 240

Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His His
245 250 255

50 Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu Ala
260 265 270

Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln Leu
275 280 285

55 Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser Phe His Pro
290 295 300

172
Leu Gly Met Ser Gly Ala Gly Ser Xaa
305 310

5 (2) INFORMATION FOR SEQ ID NO:15:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser Val Met Asn
1 5 10 15

25 His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp
20 25 30

30 Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp
35 40 45

35 Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Glu Gly Thr Leu Ser Arg
50 55 60

40 (2) INFORMATION FOR SEQ ID NO:16:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Arg Cys Lys Glu Lys Leu Asn Ser Leu Ala Ile Ser Val Met Asn
1 5 10 15

60 Met Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp
20 25 30

65 Gly Asn His Phe Glu Asp Ser Leu His Tyr Glu Gly Arg Ala Val Asp
35 40 45

70 Ile Thr Thr Ser Ser Asp Arg Asp Arg Asn Lys Tyr Glu Met Phe Ala
50 55 60

75 Arg

5 (2) INFORMATION FOR SEQ ID NO:17:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

15 (v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser Val Met Asn
1 5 10 15

20 Leu Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp
20 25 30

25 Gly Leu His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp
35 40 45

Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Arg Met Leu Ala Arg
50 55 60

30 (2) INFORMATION FOR SEQ ID NO:18:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

45 GGAATTCCCA GCAGNTGCTA AAGGAAGCAA GNGCTNAA

38

50 (2) INFORMATION FOR SEQ ID NO:19:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCATCGATGG ACCCAGATCG AAANCCNGCT CTC

33

5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

20 GCTCTAGAGC TCNACNGCNA GANCGTNGC

29

(2) INFORMATION FOR SEQ ID NO:21:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCTGTCGAC GCGGCCGCTA CGTAGGTTAC CGACGTCAAG CTTAGATCTC

50

40 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCTGAGATC TAAGCTTGAC GTCGGTAACC TACGTAGCGG CCGCGTCGAC

50

55

(2) INFORMATION FOR SEQ ID NO:23:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCGGCCAG GCAGGCCTCG CGATATCGTC ACCGCGGTAT TCGAA

45

15 (2) INFORMATION FOR SEQ ID NO:24:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGTGCCAGTC GGGGCCCCCA GGGCCGCGCC

30

35 (2) INFORMATION FOR SEQ ID NO:25:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACCAACAGCG GATGGTTCGG

20

50 (2) INFORMATION FOR SEQ ID NO:26:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTGGTGGTTA TGCCGATCGC

20

10 (2) INFORMATION FOR SEQ ID NO:27:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TAAGAGGCCT ATAAGAGGCG G

21

25 (2) INFORMATION FOR SEQ ID NO:28:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

40 AAGTCAGCCC AGAGGGAGACT

20

45 (2) INFORMATION FOR SEQ ID NO:29:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

55 Cys Gly Pro Gly Arg Gly

1

5

(2) INFORMATION FOR SEQ ID NO:30:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCAGNTGCT AAAGGAAGCA AGNGCTNAA

29

20 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTCNACNGCN AGANCKNGTN GCNA

24

35 (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGCAGGGAT CCACCATGCG GCTTTGACG AG

32

50 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGAT CCTTATTCCA CACGAGGGAT T

31

10 (2) INFORMATION FOR SEQ ID NO:34:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

25 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
1 5 10 15

30 Cys Leu Ser Leu Asp Ala Lys Cys His Ser Ser Ser Ser Ser Ser Ser
20 25 30

35 Ser Lys Ser Ala Ala Ser Ser Ile Ser Ala Ile Pro Gln Glu Glu Thr
35 40 45

40 Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
50 55 60

45 Thr Ser Leu Val Ala Leu Leu Ile Val Leu Pro Met Val Phe Ser
65 70 75 80

50 Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
85 90 95

55 Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
100 105 110

60 Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
115 120 125

65 Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
130 135 140

70 Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Arg Leu Met Ser Lys
145 150 155 160

75 Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
165 170 175

80 Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
180 185 190

179

	His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile			
	195	200	205	
5	Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu			
	210	215	220	
	Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His			
	225	230	235	240
10	Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His			
	245	250	255	
	Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg			
15	260	265	270	
	Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr			
	275	280	285	
20	Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg			
	290	295	300	
	Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly			
	305	310	315	320
25	Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro			
	325	330	335	
	Glu Ser Gln Lys Leu Thr Phe Val Phe Ala Asp Arg Ile Glu Glu Lys			
30	340	345	350	
	Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln			
	355	360	365	
35	Arg Val Val Lys Val Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro			
	370	375	380	
	Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys			
	385	390	395	400
40	Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro			
	405	410	415	
	Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln			
45	420	425	430	
	Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Asn Gly			
	435	440	445	
50	Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu			
	450	455	460	
	Pro Gln Ser Trp Arg His Asp			
	465	470		

55

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Cys Lys Glu Arg Val Asn Ser Leu Ala Ile Ala Val Met His Met
1 5 10 15

15 Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly
20 25 30

20 His His Leu Pro Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile
35 40 45

Thr Thr Ser Asp Arg Asp Arg His Lys Tyr Gly Met Leu Ala Arg Leu
50 55 60

25 Ala Val Glu Ala Gly Phe Asp Trp Val
65 70

(2) INFORMATION FOR SEQ ID NO:36:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser Val Met Asn Gln
45 1 5 10 15

Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly
20 25 30

50 His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile
35 40 45

Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met Leu Ala Arg Leu
50 55 60

55 Ala Val Glu Ala Gly Phe Asp Trp Val
65 70

(2) INFORMATION FOR SEQ ID NO:37:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Lys Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn
1 5 10 15

20 Glu Trp Pro Gly Ile Arg Leu Val Val Thr Glu Ser Trp Asp Glu Asp
20 25 30

Tyr His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr
35 40 45

25 Ile Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg
50 55 60

30 (2) INFORMATION FOR SEQ ID NO:38:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAAGCTTTA YTGYTAYGTN GGNATHGG

28

(2) INFORMATION FOR SEQ ID NO:39:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

AAGAATTCTA NGCRTTRTAR TTRTTNGG

5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 165 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

20

Cys	Gly	Pro	Gly	Arg	Gly	Xaa	Gly	Xaa	Arg	Arg	His	Pro	Lys	Lys	Leu
1	5													15	

25

Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr
	20							25					30		

30

Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Xaa	Arg	Asn	Ser	Glu
	35						40					45			

35

Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys
	50					55					60				

40

Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys
	65					70				75			80		

45

Asp	Lys	Leu	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	Pro	Gly
	85						90					95			

50

Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Xaa
		100				105					110				

55

Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser
	115					120					125				

60

Asp	Arg	Asp	Xaa	Ser	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	Val	Glu
	130					135					140				

65

Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys
	145					150				155			160		

70

Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe
	165						170			175					

75

Pro	Gly	Ser	Ala	Xaa	Val	Xaa	Leu	Xaa	Xaa	Gly	Gly	Xaa	Lys	Xaa	Val
	180					185				190					

Lys	Asp	Leu	Xaa	Pro	Gly	Asp	Xaa	Val	Leu	Ala	Ala	Asp	Xaa	Xaa	Gly
	195					200					205				

Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
210 215 220

5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
1 5 10 15

25 Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
35 40 45

30 Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
50 55 60

35 Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
65 70 75 80

Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
85 90 95

40 Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
100 105 110

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
115 120 125

45 Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
130 135 140

50 Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
145 150 155 160

His Xaa Ser Val Lys Xaa Xaa
165

55

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

10 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3897

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG GAC CGC GAC AGC CTC CCA CGC GTT CCG GAC ACA CAC GGC GAT GTG	48
Met Asp Arg Asp Ser Leu Pro Arg Val Pro Asp Thr His Gly Asp Val	
1 5 10 15	
20 GTC GAT GAG AAA TTA TTC TCG GAT CTT TAC ATA CGC ACC AGC TGG GTG	96
Val Asp Glu Lys Leu Phe Ser Asp Leu Tyr Ile Arg Thr Ser Trp Val	
20 25 30	
25 GAC GCC CAA GTG GCG CTC GAT CAG ATA GAT AAG GGC AAA GCG CGT GGC	144
Asp Ala Gln Val Ala Leu Asp Gln Ile Asp Lys Gly Lys Ala Arg Gly	
35 40 45	
30 AGC CGC ACG GCG ATC TAT CTG CGA TCA GTA TTC CAG TCC CAC CTC GAA	192
Ser Arg Thr Ala Ile Tyr Leu Arg Ser Val Phe Gln Ser His Leu Glu	
50 55 60	
35 ACC CTC GGC AGC TCC GTG CAA AAG CAC GCG GGC AAG GTG CTA TTC GTG	240
Thr Leu Gly Ser Ser Val Gln Lys His Ala Gly Lys Val Leu Phe Val	
65 70 75 80	
40 GCT ATC CTG GTG CTG AGC ACC TTC TGC GTC GGC CTG AAG AGC GCC CAG	288
Ala Ile Leu Val Leu Ser Thr Phe Cys Val Gly Leu Lys Ser Ala Gln	
85 90 95	
45 ATC CAC TCC AAG GTG CAC CAG CTG TGG ATC CAG GAG GGC GGC GGG CTG	336
Ile His Ser Lys Val His Gln Leu Trp Ile Gln Glu Gly Gly Leu	
100 105 110	
50 GAG GCG GAA CTG GCC TAC ACA CAG AAG ACG ATC GGC GAG GAC GAG TCG	384
Glu Ala Glu Leu Ala Tyr Thr Gln Lys Thr Ile Gly Glu Asp Glu Ser	
115 120 125	
55 GCC ACG CAT CAG CTG CTC ATT CAG ACG ACC CAC GAC CCG AAC GCC TCC	432
Ala Thr His Gln Leu Leu Ile Gln Thr Thr His Asp Pro Asn Ala Ser	
130 135 140	
GTC CTG CAT CCG CAG GCG CTG CTT GCC CAC CTG GAG GTC CTG GTC AAG	480
Val Leu His Pro Gln Ala Leu Leu Ala His Leu Glu Val Leu Val Lys	
145 150 155 160	
GCC ACC GCC GTC AAG GTG CAC CTC TAC GAC ACC GAA TGG GGG CTG CGC	528
Ala Thr Ala Val Lys Val His Leu Tyr Asp Thr Glu Trp Gly Leu Arg	

	165	170	175	
5	GAC ATG TGC AAC ATG CCG AGC ACG CCC TCC TTC GAG GGC ATC TAC TAC Asp Met Cys Asn Met Pro Ser Thr Pro Ser Phe Glu Gly Ile Tyr Tyr 180 185 190			576
10	ATC GAG CAG ATC CTG CGC CAC CTC ATT CCG TGC TCG ATC ATC ACG CCG Ile Glu Gln Ile Leu Arg His Leu Ile Pro Cys Ser Ile Ile Thr Pro 195 200 205			624
15	CTG GAC TGT TTC TGG GAG GGA AGC CAG CTG TTG GGT CCG GAA TCA GCG Leu Asp Cys Phe Trp Glu Gly Ser Gln Leu Leu Gly Pro Glu Ser Ala 210 215 220			672
20	GTC GTT ATA CCA GGC CTC AAC CAA CGA CTC CTG TGG ACC ACA CTG AAT Val Val Ile Pro Gly Leu Asn Gln Arg Leu Leu Trp Thr Thr Leu Asn 225 230 235 240			720
25	CCC GCC TCT GTG ATG CAG TAT ATG AAG CAG AAG ATG TCC GAG GAA AAG Pro Ala Ser Val Met Gln Tyr Met Lys Gln Lys Met Ser Glu Glu Lys 245 250 255			768
30	ATC AGC TTC GAC TTC GAG ACC GTG GAG CAG TAC ATG AAG CGT GCG GCC Ile Ser Phe Asp Phe Glu Thr Val Glu Gln Tyr Met Lys Arg Ala Ala 260 265 270			816
35	ATT GCG AGT GGC TAC ATG GAG AAG CCC TGC CTG AAC CCA CTG AAT CCC Ile Ala Ser Gly Tyr Met Glu Lys Pro Cys Leu Asn Pro Leu Asn Pro 275 280 285			864
40	AAT TGC CCG GAC ACG GCA CCG AAC AAG AAC AGC ACC CAG CCG CCG GAT Asn Cys Pro Asp Thr Ala Pro Asn Lys Asn Ser Thr Gln Pro Pro Asp 290 295 300			912
45	GTG GGA GCC ATC CTG TCC GGA GGC TGC TAC GGT TAT GCC GCG AAG CAC Val Gly Ala Ile Leu Ser Gly Gly Cys Tyr Gly Tyr Ala Ala Lys His 305 310 315 320			960
50	ATG CAC TGG CCG GAG CTG ATT GTG GGC GGA GCG AAG AGG AAC CGC Met His Trp Pro Glu Glu Leu Ile Val Gly Gly Ala Lys Arg Asn Arg 325 330 335			1008
55	AGC GGA CAC TTG AGG AAG GCC CAG GCC CTG CAG TCG GTG GTG CAG CTG Ser Gly His Leu Arg Lys Ala Gln Ala Leu Gln Ser Val Val Gln Leu 340 345 350			1056
60	ATG ACC GAG AAG GAA ATG TAC GAC CAG TGG CAG GAC AAC TAC AAG GTG Met Thr Glu Lys Glu Met Tyr Asp Gln Trp Gln Asp Asn Tyr Lys Val 355 360 365			1104
65	CAC CAT CTT GGA TGG ACG CAG GAG AAG GCA GCG GAG GTT TTG AAC GCC His His Leu Gly Trp Thr Gln Glu Lys Ala Ala Glu Val Leu Asn Ala 370 375 380			1152
70	TGG CAG CGC AAC TTT TCG CGG GAG GTG GAA CAG CTG CTA CGT AAA CAG Trp Gln Arg Asn Phe Ser Arg Glu Val Glu Gln Leu Leu Arg Lys Gln 385 390 395 400			1200

TCG AGA ATT GCC ACC AAC TAC GAT ATC TAC GTG TTC AGC TCG GCT GCA 1248
 Ser Arg Ile Ala Thr Asn Tyr Asp Ile Tyr Val Phe Ser Ser Ala Ala
 405 410 415

5 CTG GAT GAC ATC CTG GCC AAG TTC TCC CAT CCC AGC GCC TTG TCC ATT 1296
 Leu Asp Asp Ile Leu Ala Lys Phe Ser His Pro Ser Ala Leu Ser Ile
 420 425 430

10 GTC ATC GGC GTG GCC GTC ACC GTT TTG TAT GCC TTC TGC ACG CTC CTC 1344
 Val Ile Gly Val Ala Val Thr Val Leu Tyr Ala Phe Cys Thr Leu Leu
 435 440 445

15 CGC TGG AGG GAC CCC GTC CGT GGA CAG AGC AGT GTC GGC GTG GCC GGA 1392
 Arg Trp Arg Asp Pro Val Arg Gly Gln Ser Ser Val Gly Val Ala Gly
 450 455 460

20 GTT CTG CTC ATG TGC TTT AGT ACC GCC GCC GGA TTG GGA TTG TCA GCC 1440
 Val Leu Leu Met Cys Phe Ser Thr Ala Ala Gly Leu Gly Leu Ser Ala
 465 470 475 480

25 CTG CTC GGT ATC GTT TTC AAT GCC GCC AGC ACC CAG GTG GTT CCG TTT 1488
 Leu Leu Gly Ile Val Phe Asn Ala Ala Ser Thr Gln Val Val Pro Phe
 485 490 495

30 TTG GCC CTT GGT CTG GGC GTC GAT CAC ATC TTC ATG CTG ACC GCT GCC 1536
 Leu Ala Leu Gly Leu Gly Val Asp His Ile Phe Met Leu Thr Ala Ala
 500 505 510

35 TAT GCG GAG AGC AAT CGG CGG GAG CAG ACC AAG CTG ATT CTC AAG AAA 1584
 Tyr Ala Glu Ser Asn Arg Arg Glu Gln Thr Lys Leu Ile Leu Lys Lys
 515 520 525

40 GTG GGA CCG AGC ATC CTG TTC AGT GCC TGC AGC ACC GCA GGA TCC TTC 1632
 Val Gly Pro Ser Ile Leu Phe Ser Ala Cys Ser Thr Ala Gly Ser Phe
 530 535 540

45 TTT GCG GCC GCC TTT ATT CCG GTG CCG GCT TTG AAG GTA TTC TGT CTG 1680
 Phe Ala Ala Ala Phe Ile Pro Val Pro Ala Leu Lys Val Phe Cys Leu
 545 550 555 560

50 CAG GCT GCC ATC GTA ATG TGC TCC AAT TTG GCA GCG GCT CTA TTG GTT 1728
 Gln Ala Ala Ile Val Met Cys Ser Asn Leu Ala Ala Ala Leu Leu Val
 565 570 575

55 TTT CCG GCC ATG ATT TCG TTG GAT CTA CGG AGA CGT ACC GCC GGC AGG 1776
 Phe Pro Ala Met Ile Ser Leu Asp Leu Arg Arg Arg Thr Ala Gly Arg
 580 585 590

50 GCG GAC ATC TTC TGC TGC TGT TTT CCG GTG TGG AAG GAA CAG CCG AAG 1824
 Ala Asp Ile Phe Cys Cys Phe Pro Val Trp Lys Glu Gln Pro Lys
 595 600 605

55 GTG GCA CCA CCG GTG CTG CCG CTG AAC AAC AAC AAC GGG CGC GGG GCC 1872
 Val Ala Pro Pro Val Leu Pro Leu Asn Asn Asn Gly Arg Gly Ala
 610 615 620

CGG CAT CCG AAG AGC TGC AAC AAC AAC AGG GTG GCG CTG CCC GCC CAG 1920
 Arg His Pro Lys Ser Cys Asn Asn Asn Arg Val Ala Leu Pro Ala Gln

	625	630	635	640	
	AAT CCT CTG CTG GAA CAG AGG GCA GAC ATC CCT GGG AGC AGT CAC TCA Asn Pro Leu Leu Glu Gln Arg Ala Asp Ile Pro Gly Ser Ser His Ser				1968
5	645		650	655	
	CTG GCG TCC TTC TCT CTG GCA ACA TTC GCC TTT CAG CAC TAC ACT CCC Leu Ala Ser Phe Ser Leu Ala Thr Phe Ala Phe Gln His Tyr Thr Pro				2016
	660	665		670	
10	TTC CTC ATG CGC AGC TGG GTG AAG TTC CTG ACC GTT ATG GGT TTC CTG Phe Leu Met Arg Ser Trp Val Lys Phe Leu Thr Val Met Gly Phe Leu				2064
	675	680	685		
15	GCG GCC CTC ATA TCC AGC TTG TAT GCC TCC ACG CGC CTT CAG GAT GGC Ala Ala Leu Ile Ser Ser Leu Tyr Ala Ser Thr Arg Leu Gln Asp Gly				2112
	690	695	700		
20	CTG GAC ATT ATT GAT CTG GTG CCC AAG GAC AGC AAC GAG CAC AAG TTC Leu Asp Ile Ile Asp Leu Val Pro Lys Asp Ser Asn Glu His Lys Phe				2160
	705	710	715	720	
25	CTG GAT GCT CAA ACT CGG CTC TTT GCC TTC TAC AGC ATG TAT GCG GTT Leu Asp Ala Gln Thr Arg Leu Phe Gly Phe Tyr Ser Met Tyr Ala Val				2208
	725	730		735	
	ACC CAG GGC AAC TTT GAA TAT CCC ACC CAG CAG CAG TTG CTC AGG GAC Thr Gln Gly Asn Phe Glu Tyr Pro Thr Gln Gln Gln Leu Leu Arg Asp				2256
	740	745		750	
30	TAC CAT GAT TCC TTT GTG CGG GTG CCA CAT GTG ATC AAG AAT GAT AAT Tyr His Asp Ser Phe Val Arg Val Pro His Val Ile Lys Asn Asp Asn				2304
	755	760	765		
35	GGT GGA CTG CCG GAC TTC TGG CTG CTC TTC AGC GAG TGG CTG GGT Gly Gly Leu Pro Asp Phe Trp Leu Leu Leu Phe Ser Glu Trp Leu Gly				2352
	770	775	780		
40	AAT CTG CAA AAG ATA TTC GAC GAG GAA TAC CGC GAC GGA CGG CTG ACC Asn Leu Gln Lys Ile Phe Asp Glu Glu Tyr Arg Asp Gly Arg Leu Thr				2400
	785	790	795	800	
	AAG GAG TGC TGG TTC CCA AAC GCC AGC AGC GAT GCC ATC CTG GCC TAC Lys Glu Cys Trp Phe Pro Asn Ala Ser Ser Asp Ala Ile Leu Ala Tyr				2448
45	805	810		815	
	AAG CTA ATC GTG CAA ACC GGC CAT GTG GAC AAC CCC GTG GAC AAG GAA Lys Leu Ile Val Gln Thr Gly His Val Asp Asn Pro Val Asp Lys Glu				2496
	820	825		830	
50	CTG GTG CTC ACC AAT CGC CTG GTC AAC AGC GAT GGC ATC ATC AAC CAA Leu Val Leu Thr Asn Arg Leu Val Asn Ser Asp Gly Ile Ile Asn Gln				2544
	835	840	845		
55	CGC GCC TTC TAC AAC TAT CTG TCG GCA TGG GCC ACC AAC GCG TCT TCG Arg Ala Phe Tyr Asn Tyr Leu Ser Ala Trp Ala Thr Asn Ala Ser Ser				2592
	850	855	860		

	CCT ACG GAG CTT CTC AGG GCA AAT TGT ATC CGG AAC CGC GCC AAC GGA Pro Thr Glu Leu Leu Arg Ala Asn Cys Ile Arg Asn Arg Ala Asn Gly 865 870 875 880	2640
5	GCT TCT CAG GGC AAA TTG TAT CCG GAA CCG CGC CAG TAT TTT CAC CAA Ala Ser Gln Gly Lys Leu Tyr Pro Glu Pro Arg Gln Tyr Phe His Gln 885 890 895	2688
10	CCC AAC GAG TAC GAT CTT AAG ATA CCC AAG AGT CTG CCA TTG GTC TAC Pro Asn Glu Tyr Asp Leu Lys Ile Pro Lys Ser Leu Pro Leu Val Tyr 900 905 910	2736
15	GCT CAG ATG CCC TTT TAC CTC CAC GGA CTA ACA GAT ACC TCG CAG ATC Ala Gln Met Pro Phe Tyr Leu His Gly Leu Thr Asp Thr Ser Gln Ile 915 920 925	2784
	AAG ACC CTG ATA GGT CAT ATT CGC GAC CTG AGC GTC AAG TAC GAG GGC Lys Thr Leu Ile Gly His Ile Arg Asp Leu Ser Val Lys Tyr Glu Gly 930 935 940	2832
20	TTC GGC CTG CCC AAC TAT CCA TCG GGC ATT CCC TTC ATC TTC TGG GAG Phe Gly Leu Pro Asn Tyr Pro Ser Gly Ile Pro Phe Ile Phe Trp Glu 945 950 955 960	2880
25	CAG TAC ATG ACC CTG CGC TCC TCA CTG GCC ATG ATC CTG GCC TGC GTG Gln Tyr Met Thr Leu Arg Ser Ser Leu Ala Met Ile Leu Ala Cys Val 965 970 975	2928
30	CTA CTC GCC CTG GTG CTG GTC TCC CTG CTC CTG CTC TCC GTT TGG Leu Leu Ala Ala Leu Val Leu Val Ser Leu Leu Leu Ser Val Trp 980 985 990	2976
	GCC GCC GTT CTC GTG ATC CTC AGC GTT CTG GCC TCG CTG GCC CAG ATC Ala Ala Val Leu Val Ile Leu Ser Val Leu Ala Ser Leu Ala Gln Ile 995 1000 1005	3024
35	TTT GGG GCC ATG ACT CTG CTG GGC ATC AAA CTC TCG GCC ATT CCG GCA Phe Gly Ala Met Thr Leu Leu Gly Ile Lys Leu Ser Ala Ile Pro Ala 1010 1015 1020	3072
40	GTC ATA CTC ATC CTC AGC GTG GGC ATG ATG CTG TGC TTC AAT GTG CTG Val Ile Leu Ile Leu Ser Val Gly Met Met Leu Cys Phe Asn Val Leu 1025 1030 1035 1040	3120
45	ATA TCA CTG GGC TTC ATG ACA TCC GTT GGC AAC CGA CAG CGC CGC GTC Ile Ser Leu Gly Phe Met Thr Ser Val Gly Asn Arg Gln Arg Arg Val 1045 1050 1055	3168
50	CAG CTG AGC ATG CAG ATG TCC CTG GGA CCA CTT GTC CAC GGC ATG CTG Gln Leu Ser Met Gln Met Ser Leu Gly Pro Leu Val His Gly Met Leu 1060 1065 1070	3216
	ACC TCC GGA GTG GCC GTG TTC ATG CTC TCC ACG TCG CCC TTT GAG TTT Thr Ser Gly Val Ala Val Phe Met Leu Ser Thr Ser Pro Phe Glu Phe	3264
55	1075 1080 1085	
	GTG ATC CGG CAC TTC TGC TGG CTT CTG CTG GTG GTC TTA TGC GTT GGC Val Ile Arg His Phe Cys Trp Leu Leu Val Val Leu Cys Val Gly	3312

	1090	1095	1100	
5	GCC TGC AAC AGC CTT TTG GTG TTC CCC ATC CTA CTG AGC ATG GTG GGA Ala Cys Asn Ser Leu Leu Val Phe Pro Ile Leu Leu Ser Met Val Gly 1105 1110 1115 1120			3360
10	CCG GAG GCG GAG CTG GTG CCG CTG GAG CAT CCA GAC CGC ATA TCC ACG Pro Glu Ala Glu Leu Val Pro Leu Glu His Pro Asp Arg Ile Ser Thr 1125 1130 1135			3408
15	CCC TCT CCG CTG CCC GTG CGC AGC AGC AAG AGA TCG GGC AAA TCC TAT Pro Ser Pro Leu Pro Val Arg Ser Ser Lys Arg Ser Gly Lys Ser Tyr 1140 1145 1150			3456
20	GTG GTG CAG GGA TCG CGA TCC TCG CGA GGC AGC TGC CAG AAG TCG CAT Val Val Gln Gly Ser Arg Ser Arg Gly Ser Cys Gln Lys Ser His 1155 1160 1165			3504
25	CAC CAC CAC AAA GAC CTT AAT GAT CCA TCG CTG ACG ACG ATC ACC His His His Lys Asp Leu Asn Asp Pro Ser Leu Thr Thr Ile Thr 1170 1175 1180			3552
30	GAG GAG CCG CAG TCG TGG AAG TCC AGC AAC TCG TCC ATC CAG ATG CCC Glu Glu Pro Gln Ser Trp Lys Ser Ser Asn Ser Ser Ile Gln Met Pro 1185 1190 1195 1200			3600
35	AAT GAT TGG ACC TAC CAG CCG CGG GAA CAG CGA CCC GCC TCC TAC GCG Asn Asp Trp Thr Tyr Gln Pro Arg Glu Gln Arg Pro Ala Ser Tyr Ala 1205 1210 1215			3648
40	GCC CCG CCC CCC GCC TAT CAC AAG GCC GCC CAG CAC CAC CAG Ala Pro Pro Pro Ala Tyr His Lys Ala Ala Gln Gln His His Gln 1220 1225 1230			3696
45	CAT CAG GGC CCG CCC ACA ACG CCC CCG CCC TTC CCG ACG GCC TAT His Gln Gly Pro Pro Thr Thr Pro Pro Pro Pro Phe Pro Thr Ala Tyr 1235 1240 1245			3744
50	CCG CCG GAG CTG CAG AGC ATC GTG GTG CAG CCG GAG GTG ACG GTG GAG Pro Pro Glu Leu Gln Ser Ile Val Val Gln Pro Glu Val Thr Val Glu 1250 1255 1260			3792
55	ACG ACG CAC TCG GAC AGC AAC ACC ACC AAG GTG ACG GCC ACG GCC AAC Thr Thr His Ser Asp Ser Asn Thr Thr Lys Val Thr Ala Thr Ala Asn 1265 1270 1275 1280			3840
60	ATC AAG GTG GAG CTG GCC ATG CCC GGC AGG GCG GTG CGC AGC TAT AAC Ile Lys Val Glu Leu Ala Met Pro Gly Arg Ala Val Arg Ser Tyr Asn 1285 1290 1295			3888
65	TTT ACG AGT TAG Phe Thr Ser			3900

55 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCGAGGGCT GGGACGAAGA TGGC

24

15 (2) INFORMATION FOR SEQ ID NO:44:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGCTCGGTCTG TACGGCATGA ACGAC

25

30 (2) INFORMATION FOR SEQ ID NO:45:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

45 ATGGGGATGT GTGTGTGGTC AAGTGT

27

(2) INFORMATION FOR SEQ ID NO:46:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TTCACAGACT CTCAAAGTGT ATTTT

25

5

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

20

Met Gly Ser Ser His His His His His Leu Val Pro Arg Gly Ser
1 5 10 15

His Met

25